This Raw Listing contains the General Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo

(ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC ACIDS ENCODING THE RECEPTOR, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 54

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: David A. Jackson, Esq.
(B) STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/586,594
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-162

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 201-487-5800
(B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2529 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGCTCAGGT CGGCGTCGTA CCAGCCGCTG AAGCGGTTCT CCAGGTTCCA GGCGCTCTCG 60

CCATGCCGGA TCAGCACCAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG TTGCTTTGGG 120

AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA GACACTGGCT 180

TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT AGAGTGCTGG 240

ATGAAAGGGG ACTTGACATT ATTCATCTGT CATATGGAGC CATTACCTAA GAACCCCTTC 300

AAGAATTATG ACTCTAAGGT CCATCTTTTA TATGATCTGC CTGAAGTCAT AGATGATTCG 360

CCTCTGCCCC CACTGAAAGA CAGCTTTCAG ACTGTCCAAT GCAACTGCAG TCTTCGGGGA 420

TGTGAATGTC ATGTGCCGGT ACCCAGAGCC AAACTCAACT ACGCTCTTCT GATGTATTTG 480

GAAATCACAT CTGCCGGTGT GAGTTTTCAG TCACCTCTGA TGTCACTGCA GCCCATGCTT 540

GTTGTGAAAC CCGATCCACC CTTAGGTTTG CATATGGAAG TCACAGATGA TGGTAATTTA 600

AAGATTTCTT GGGACAGCCA AACAATGGCA CCATTTCCGC TTCAATATCA GGTGAAATAT 660

TTAGAGAATT CTACAATTGT AAGAGAGGCT GCTGAAATTG TCTCAGCTAC ATCTCTGCTG 720

GTAGACAGTG TGCTTCCTGG ATCTTCATAT GAGGTCCAGG TGAGGAGCAA GAGACTGGAT 780

GGTTCAGGAG TCTGGAGTGA CTGGAGTTCA CCTCAAGTCT TTACCACACA AGATGTTGTG 840

TATTTTCCAC CCAAAATTCT GACTAGTGTT GGATCGAATG CTTCTTTTCA TTGCATCTAC 900

AAAAACGAAA ACCAGATTAT CTCCTCAAAA CAGATAGTTT GGTGGAGGAA TCTAGCTGAG 960

AAAATCCCTG AGATACAGTA CAGCATTGTG AGTGACCGAG TTAGCAAAGT TACCTTCTCC 1020

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100  AACCTGAAAG CCACCAGACC TCGAGGGAAG TTTACCTATG ACGCAGTGTA CTGCTGCAAT   1080
101
102  GAGCAGGCGT GCCATCACCG CTATGCTGAA TTATACGTGA TCGATGTCAA TATCAATATA   1140
103
104  TCATGTGAAA CTGACGGGTA CTTAACTAAA ATGACTTGCA GATGGTCACC CAGCACAATC   1200
105
106  CAATCACTAG TGGGAAGCAC TGTGCAGCTG AGGTATCACA GGCGCAGCCT GTATTGTCCT   1260
107
108  GATAGTCCAT CTATTCATCC TACGTCTGAG CCCAAAAACT GCGTCTTACA GAGAGACGGC   1320
109
110  TTTTATGAAT GTGTTTTCCA GCCAATCTTT CTATTATCTG GCTATACAAT GTGGATCAGG   1380
111
112  ATCAACCATT CTTTAGGTTC ACTTGACTCG CCACCAACGT GTGTCCTTCC TGACTCCGTA   1440
113
114  GTAAAACCAC TACCTCCATC TAACGTAAAA GCAGAGATTA CTGTAAACAC TGGATTATTG   1500
115
116  AAAGTATCTT GGGAAAAGCC AGTCTTTCCG GAGAATAACC TTCAATTCCA GATTCGATAT   1560
117
118  GGCTTAAGTG GAAAAGAAAT ACAATGGAAG ACACATGAGG TATTCGATGC AAAGTCAAAG   1620
119
120  TCTGCCAGCC TGCTGGTGTC AGACCTCTGT GCAGTCTATG TGGTCCAGGT TCGCTGCCGG   1680
121
122  CGGTTGGATG GACTAGGATA TTGGAGTAAT TGGAGCAGTC CAGCCTATAC GCTTGTCATG   1740
123
124  GATGTAAAAG TTCCTATGAG AGGGCCTGAA TTTTGGAGAA AAATGGATGG GGACGTTACT   1800
125
126  AAAAAGGAGA GAAATGTCAC CTTGCTTTGG AAGCCCCTGA CGAAAAATGA CTCACTGTGT   1860
127
128  AGTGTGAGGA GGTACGTGGT GAAGCATCGT ACTGCCCACA ATGGGACGTG GTCAGAAGAT   1920
129
130  GTGGGAAATC GGACCAATCT CACTTTCCTG TGGACAGAAC CAGCGCACAC TGTTACAGTT   1980
131
132  CTGGCTGTCA ATTCCCTCGG CGCTTCCCTT GTGAATTTTA ACCTTACCTT CTCATGGCCC   2040
133
134  ATGAGTAAAG TGAGTGCTGT GGAGTCACTC AGTGCTTATC CCCTGAGCAG CAGCTGTGTC   2100
135
136  ATCCTTTCCT GGACACTGTC ACCTGATGAT TATAGTCTGT TATATCTGGT TATTGAATGG   2160
137
138  AAGATCCTTA ATGAAGATGA TGGAATGAAG TGGCTTAGAA TTCCCTCGAA TGTTAAAAAG   2220
139
140  TTTTATATCC ACGATAATTT TATTCCCATC GAGAAATATC AGTTTAGTCT TTACCCAGTA   2280
141
142  TTTATGGAAG GAGTTGGAAA ACCAAAGATA ATTAATGGTT TCACCAAAGA TGCTATCGAC   2340
143
144  AAGCAGCAGA ATGACGCAGG GCTGTATGTC ATTGTACCCA TAATTATTTC CTCTTGTGTC   2400
145
146  CTACTGCTCG GAACACTGTT AATTTCACAC CAGAGAATGA AAAAGTTGTT TTGGGACGAT   2460
147
148  GTTCCAAACC CCAAGAATTG TTCCTGGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC   2520
149
150  ACTCTTTGA                                                           2529
151
152  (2) INFORMATION FOR SEQ ID NO:2:
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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 842 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: Not Relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly Leu Arg Ser Ala Ser Tyr Gln Pro Leu Lys Arg Phe Ser Arg Phe
1 5 10 15

Gln Ala Leu Ser Pro Cys Arg Ile Ser Thr Ser Leu Xaa Leu Val Pro
20 25 30

Asn Ser Ala Arg Gly Cys Phe Gly Asn Glu Gln Gly Gln Asn Cys Ser
35 40 45

Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala Ser Val Val Lys
50 55 60

Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp Ile Glu Cys Trp
65 70 75 80

Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met Glu Pro Leu Pro
85 90 95

Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His Leu Leu Tyr Asp
100 105 110

Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro Leu Lys Asp Ser
115 120 125

Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His
130 135 140

Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu Leu Met Tyr Leu
145 150 155 160

Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu
165 170 175

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206
207     Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu His Met
208                 180                 185                 190
209
210     Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr
211             195                 200                 205
212
213     Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser
214         210                 215                 220
215
216     Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala Thr Ser Leu Leu
217     225                 230                 235                 240
218
219     Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser
220                     245                 250                 255
221
222     Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Ser Pro Gln
223                 260                 265                 270
224
225     Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro Lys Ile Leu Thr
226             275                 280                 285
227
228     Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr Lys Asn Glu Asn
229         290                 295                 300
230
231     Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg Asn Leu Ala Glu
232     305                 310                 315                 320
233
234     Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys
235                     325                 330                 335
236
237     Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr
238                 340                 345                 350
239
240     Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr
241             355                 360                 365
242
243     Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr
244         370                 375                 380
245
246     Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile
247     385                 390                 395                 400
248
249     Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser
250                     405                 410                 415
251
252     Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys
253                 420                 425                 430
254
255     Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro
256             435                 440                 445
257
258     Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser
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